

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/303,232

DATE: 05/10/1999

TIME: 15:29:15

Input Set: I303232.RAW

This Raw Listing contains the General
 Information Section and those Sequences
 containing ERRORS.

Does Not Comply
 Corrected Diskette Needed

E--> 1 <110> Bayer Aktiengesellschaft
 2 <120> Nucleic acids which encode
 3 insect acetylcholine receptor subunits
 4 <130> Le A 33 020-Foreign Countries
 5 <140> US/09/303,232
 6 <141> 1999-04-30
 7 <150> DE-198 19 829.9
 8 <151> 1998-05-04
 9 <160> 6
 10 <170> PatentIn Ver. 2.1

3 shown in file (see p 7-18)

ERRORED SEQUENCES FOLLOW

Sequence 2 missing

E--> 11 <210> 3
 12 <211> 3701
 13 <212> DNA
 14 <213> Heliothis virescens
 15 <220>
 16 <221> CDS
 17 <222> (335) .. (1822)
 18 <400> 3
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 20 gccgtgactc cacacacatc ccctcggcgc agtaggcgat gtttgaggat cggacggcac 120
 21 gcgtggccgt cggcgagcgg tcgtgaacaa gttgcataca tatgaaaacc gtaaaaagat 180
 22 tgaatttttaa gccgatcgtg ttcgatagat cctaataagag aagcgggagt gcggcgcttg 240
 23 gtaggcgggg gtcgagtcgc gcggtcgggg gaaatggcgc ggcgcggggc ggcgcgggcg 300
 24 gcggcgcgcg gcgcgggcgc gtcgcggcgc tgac atg ggc ggg cgg gcg cgc cgc 355
 25 Met Gly Gly Arg Ala Arg Arg
 26 1 5
 27 tcg cac ttg gcg gcg ccc gcg ggc ctg ctg ctg ctg ctg tgc ctg ctc 403
 28 Ser His Leu Ala Ala Pro Ala Gly Leu Leu Leu Leu Leu Cys Leu Leu
 29 10 15 20
 30 tgg ccg agg ggg gca cgc tgc ggg tac cac gag aag cgg cta ctg cac 451
 31 Trp Pro Arg Gly Ala Arg Cys Gly Tyr His Glu Lys Arg Leu Leu His
 32 25 30 35
 33 cac cta ttg gac cac tac aac gta ctg gag agg ccc gtc gtc aac gag 499
 34 His Leu Leu Asp His Tyr Asn Val Leu Glu Arg Pro Val Val Asn Glu
 35 40 45 50 55
 36 agc gac ccg ctg cag ctc tcc ttc ggc ctc acg ctc atg cag atc atc 547
 37 Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile
 38 60 65 70
 39 gac gtg gac gag aag aac cag ctt tta ata aca aac atc tgg cta aaa 595

Please review the
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
 <223> fields of each sequence which presents at least one n r Xaa.

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40	Asp	Val	Asp	Glu	Lys	Asn	Gln	Leu	Leu	Ile	Thr	Asn	Ile	Trp	Leu	Lys	
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42	cta	gag	tgg	aat	gat	atg	aac	ttg	agg	tgg	aac	act	tca	gat	ttc	ggc	643
43	Leu	Glu	Trp	Asn	Asp	Met	Asn	Leu	Arg	Trp	Asn	Thr	Ser	Asp	Phe	Gly	
44			90					95					100				
45	ggg	gtc	aaa	gat	tta	aga	gtg	cca	ccc	cac	aga	cta	tgg	aaa	cca	gac	691
46	Gly	Val	Lys	Asp	Leu	Arg	Val	Pro	Pro	His	Arg	Leu	Trp	Lys	Pro	Asp	
47		105					110					115					
48	gtc	ctt	atg	tac	aac	agc	gcg	gac	gaa	ggg	ttc	gac	agc	acg	tat	cca	739
49	Val	Leu	Met	Tyr	Asn	Ser	Ala	Asp	Glu	Gly	Phe	Asp	Ser	Thr	Tyr	Pro	
50	120					125					130				135		
51	acg	aac	gtg	gtg	gtg	cgg	aac	aac	ggc	tcg	tgt	ctg	tac	gtg	ccg	ccc	787
52	Thr	Asn	Val	Val	Val	Arg	Asn	Asn	Gly	Ser	Cys	Leu	Tyr	Val	Pro	Pro	
53				140					145					150			
54	ggc	atc	ttc	aag	agc	acc	tgc	aag	atc	gac	atc	acc	tgg	ttc	ccc	ttc	835
55	Gly	Ile	Phe	Lys	Ser	Thr	Cys	Lys	Ile	Asp	Ile	Thr	Trp	Phe	Pro	Phe	
56			155					160					165				
57	gac	gac	caa	cga	tgc	gag	atg	aag	ttt	ggc	agc	tgg	act	tat	gat	ggt	883
58	Asp	Asp	Gln	Arg	Cys	Glu	Met	Lys	Phe	Gly	Ser	Trp	Thr	Tyr	Asp	Gly	
59			170				175					180					
60	tat	cag	ttg	gat	cta	caa	cta	cag	gat	gaa	ggg	ggc	gga	gat	ata	agc	931
61	Tyr	Gln	Leu	Asp	Leu	Gln	Leu	Gln	Asp	Glu	Gly	Gly	Gly	Asp	Ile	Ser	
62		185				190					195						
63	agt	ttt	gtc	acg	aat	ggc	gaa	tgg	gag	tta	ata	gga	gtc	ccc	ggc	aag	979
64	Ser	Phe	Val	Thr	Asn	Gly	Glu	Trp	Glu	Leu	Ile	Gly	Val	Pro	Gly	Lys	
65	200					205					210				215		
66	cgc	aac	gag	atc	tac	tac	aac	tgt	tgt	ccg	gag	cca	tac	atc	gac	atc	1027
67	Arg	Asn	Glu	Ile	Tyr	Tyr	Asn	Cys	Cys	Pro	Glu	Pro	Tyr	Ile	Asp	Ile	
68				220					225				230				
69	acg	ttt	gcg	gtg	gtg	atc	cgg	agg	aaa	acg	ctc	tac	tac	ttc	ttc	aat	1075
70	Thr	Phe	Ala	Val	Val	Ile	Arg	Arg	Lys	Thr	Leu	Tyr	Tyr	Phe	Phe	Asn	
71			235					240					245				
72	ctg	atc	gtg	ccc	tgc	gtg	ctc	atc	gcc	tcc	atg	gct	cta	ttg	ggg	ttc	1123
73	Leu	Ile	Val	Pro	Cys	Val	Leu	Ile	Ala	Ser	Met	Ala	Leu	Leu	Gly	Phe	
74			250				255					260					
75	acc	ttg	cct	cca	gac	tcc	gga	gaa	aag	ttg	tct	tta	ggt	gtg	acg	ata	1171
76	Thr	Leu	Pro	Pro	Asp	Ser	Gly	Glu	Lys	Leu	Ser	Leu	Gly	Val	Thr	Ile	
77		265				270					275						
78	tta	ctg	tcg	ttg	acg	gtg	ttc	ctc	aac	atg	gtg	gcg	gag	acg	atg	cca	1219
79	Leu	Leu	Ser	Leu	Thr	Val	Phe	Leu	Asn	Met	Val	Ala	Glu	Thr	Met	Pro	
80	280					285				290					295		
81	gcg	acg	tcg	gac	gcc	gtg	ccc	ttg	ctc	ggc	acc	tac	ttc	aac	tgc	atc	1267
82	Ala	Thr	Ser	Asp	Ala	Val	Pro	Leu	Leu	Gly	Thr	Tyr	Phe	Asn	Cys	Ile	
83				300					305				310				
84	atg	ttc	atg	gtg	gct	tcc	tcc	gtc	gtc	tcc	acc	ata	ctg	atc	ctc	aac	1315
85	Met	Phe	Met	Val	Ala	Ser	Ser	Val	Val	Ser	Thr	Ile	Leu	Ile	Leu	Asn	
86			315					320				325					
87	tac	cac	cac	cgg	cac	gca	gac	act	cac	gaa	atg	agt	gat	tgg	att	cgt	1363
88	Tyr	His	His	Arg	His	Ala	Asp	Thr	His	Glu	Met	Ser	Asp	Trp	Ile	Arg	
89			330				335					340					

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90	tgc gtg ttc ctt tat tgg ctg ccg tgg gtg ctg cgc atg tca cgg ccc	1411
91	Cys Val Phe Leu Tyr Trp Leu Pro Trp Val Leu Arg Met Ser Arg Pro	
92	345 350 355	
93	ggc tgc gcg acg acg ccg ccg ccg gcg cgc gta cct ccg ccg ccg gac	1459
94	Gly Ser Ala Thr Thr Pro Pro Pro Ala Arg Val Pro Pro Pro Pro Asp	
95	360 365 370 375	
96	ctg gag ctg cgc gag cgc tcc tcc aag tgc ctc cta gcg aac gtg ctc	1507
97	Leu Glu Leu Arg Glu Arg Ser Ser Lys Ser Leu Leu Ala Asn Val Leu	
98	380 385 390	
99	gac atc gat gac gac ttc cgc cac ccg caa gcg cag cag ccg caa tgc	1555
100	Asp Ile Asp Asp Asp Phe Arg His Pro Gln Ala Gln Gln Pro Gln Cys	
101	395 400 405	
102	tgc cga tac tac agg ggg ggt gag gag aat ggc gcg ggg ttg gcg gcg	1603
103	Cys Arg Tyr Tyr Arg Gly Gly Glu Glu Asn Gly Ala Gly Leu Ala Ala	
104	410 415 420	
105	cac agt tgc ttc ggt gtc gac tac gag ctc tcc ctc att ctg aag gag	1651
106	His Ser Cys Phe Gly Val Asp Tyr Glu Leu Ser Leu Ile Leu Lys Glu	
107	425 430 435	
108	att aga gtc atc aca gat cag atg cgc aag gac gac gaa gat gcg gac	1699
109	Ile Arg Val Ile Thr Asp Gln Met Arg Lys Asp Asp Glu Asp Ala Asp	
110	440 445 450 455	
111	att tgc cgc gac tgg aag ttc gcc gcc atg gtc gtg gac aga ctg tgc	1747
112	Ile Ser Arg Asp Trp Lys Phe Ala Ala Met Val Val Asp Arg Leu Cys	
113	460 465 470	
114	ctt att atc ttt acc ctg ttc aca atc atc gcc acg cta gcc gtg ctg	1795
115	Leu Ile Ile Phe Thr Leu Phe Thr Ile Ile Ala Thr Leu Ala Val Leu	
116	475 480 485	
117	ctg tcc gcg cca cac atc atg gtg tgc tagcgaccgc cccgcttgcg	1842
118	Leu Ser Ala Pro His Ile Met Val Ser	
119	490 495	
120	gatacgcgatg cgaaaagtgc tgtgataccg cgaatatttg ttaagttgtg atgagcgaag	1902
121	tggcgcgagc ggtgacgccg cggcgtcgga gttgccgccg cctgcctcgc cgcccgcgcc	1962
122	cccctgtaga cataagttac cgctgactgc caacctgta cgttcaacaa ataactgccc	2022
123	atccgactaa cgtcttttat ccccttgaaa aattcagcga ttgtgtaccc ctttcttcca	2082
124	agaatacaat gacaaatggt cgtcacgctc agtggaaatca atcccgactc cttcgcccgga	2142
125	tatttccctt agggatatgc acgagtttga atgagcgggt ccgtatcaga cgttccgtcc	2202
126	ccggaacggt cgtccctgc gataaagtgg cagtacgtgc tatacaggca cttaaggccg	2262
127	ccacgccacg gcgcccgggt gcgctcgggc cggaacccgc cgaccctcac cgctgcaagt	2322
128	ggccaccac tagacaagac tgcggcagaa aatatgtgca caaaaacgtc ttccttctta	2382
129	ccgatgaacg acctgattcg catttaaaat taaactttgt tagaacttct tcgattcttg	2442
130	aaatctattg tacagtttag agtttgggag gtgaaacaat ggccctttgt ttccttcttg	2502
131	ttcgattcca tgaatcgtgg ttataatccc tagttttatt ttcggatata tttgtgtcag	2562
132	tagctagtat agaactttac aaacaatgtt gattcaattg gtacagggtg tgatatgcct	2622
133	cgttgtgaac ggggtccgata ttgttataaa tggtaaaata cccatggcta tagcttaata	2682
134	aatcgttcgt taaaagtgtg agttaaaca atattatttt aataaagtca tatctgggtc	2742
135	ttccggaacg actttttacaa ataattaaat tacatatata tatcacgttt gtaacttctt	2802
136	ccatacagtt acagtaattc gtatgctgaa aataatatta gtttgtaaaa ttttcttctt	2862
137	cgaaaattta ttcaaacaga tgcgaccatc gtttcaaaca tttacatgta atatagaact	2922
138	cattttataa gatatacaac attttataag tacaagaagt tgtaacatga accggttttt	2982
139	cgttacatag aggggtataac acaaagggtc ctacatatgg acagatgcga agcacgatca	3042

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140      gttgataaagc acaggtacac tatatcctga catccgacag tcctgccgct cgtctgccac 3102
141      actcgaaaac attcgacagt tcagtttact gtcgcccat catcgattgt taagtttggt 3162
142      gttctaactc atcgcatcca tttcattcaa aaacattgta aacctctcaa ggggaaaacg 3222
143      tgttgtaaac agtgagagtg cgcgggtaca accgacacgc gaatgtaccc tcgcaaggct 3282
144      cctgtaatgt tttcctcttc cgaggtgttg ctgagagtaa tcttagacgg tccgatggaa 3342
145      gttgcggacc ggatatgatt acaagtcaat gtttttaagt catccgttta tttattgtta 3402
146      tatcttctta ccattcgcta gaggttggtg gacgacccgg acggtgggcg ccgcaaccgg 3462
147      cacacgcggg gttccatctt tgtattagat ggaagtgttg cggcatctct ccgtcggcaa 3522
148      tgggacaacc cgttggtccc aacatttggt caattgttag ggtaactct gaattgcact 3582
149      ttgtttatta aatataaacg aatgaaacaa aaaaaaaaaa aaaaaactcg agagtacttc 3642
150      tagagcgggc gcgggcccac cgattttcca cccgggtggg gtaccargta agtgatccc 3701

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E--> 151 <210> 5
 152 <211> 3109
 153 <212> DNA
 154 <213> Heliothis virescens
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 156 <221> CDS
 157 <222> (95)..(1597)
 158 <400> 5

Sequence 4 missing

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161                                     Met Ala Pro Met Leu Ala Ala
162                                     1           5
163      ttg gcg ctg ctg gct ttg ctg ccc gta tcg gag caa ggt cct cac gag 163
164      Leu Ala Leu Leu Ala Leu Leu Pro Val Ser Glu Gln Gly Pro His Glu
165      10           15           20
166      aag aga ctc ctg aac gcg ttg ctg gcg aac tac aac acc ctg gag cga 211
167      Lys Arg Leu Leu Asn Ala Leu Leu Ala Asn Tyr Asn Thr Leu Glu Arg
168      25           30           35
169      ccg gtg gcc aac gag agc gaa ccg cta gag gtc agg ttc ggc ttg acc 259
170      Pro Val Ala Asn Glu Ser Glu Pro Leu Glu Val Arg Phe Gly Leu Thr
171      40           45           50           55
172      ttg cag caa atc att gac gtg gac gag aag aat caa cta ctt ata acc 307
173      Leu Gln Gln Ile Ile Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr
174      60           65           70
175      aat ata tgg ctg tcg ttg gag tgg aat gac tac aac ctg agg tgg aac 355
176      Asn Ile Trp Leu Ser Leu Glu Trp Asn Asp Tyr Asn Leu Arg Trp Asn
177      75           80           85
178      gac agc gag tat ggc ggg gtc aag gac ctc agg atc acg ccc aac aag 403
179      Asp Ser Glu Tyr Gly Gly Val Lys Asp Leu Arg Ile Thr Pro Asn Lys
180      90           95           100
181      ttg tgg aag ccg gac gtc ctt atg tat aat agt gct gac gag ggt ttt 451
182      Leu Trp Lys Pro Asp Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe
183      105           110           115
184      gac ggg acc tac cag acc aac gtg gtg gtc aga agc ggc ggc agt tgc 499
185      Asp Gly Thr Tyr Gln Thr Asn Val Val Val Arg Ser Gly Gly Ser Cys
186      120           125           130           135
187      ctg tac gtg cca cct ggc ata ttc aag agc aca tgc aag atg gac atc 547
188      Leu Tyr Val Pro Pro Gly Ile Phe Lys Ser Thr Cys Lys Met Asp Ile

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189				140				145				150					
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191	Ala	Trp	Phe	Pro	Phe	Asp	Asp	Gln	His	Cys	Asp	Met	Lys	Phe	Gly	Ser	
192				155				160					165				
193	tgg	aca	tat	gac	ggc	aat	cag	ttg	gat	ctg	gtg	cta	aaa	gat	gag	gca	643
194	Trp	Thr	Tyr	Asp	Gly	Asn	Gln	Leu	Asp	Leu	Val	Leu	Lys	Asp	Glu	Ala	
195				170				175					180				
196	ggc	ggc	gat	cta	tcg	gac	ttc	ata	aca	aat	ggg	gag	tgg	tat	cta	ata	691
197	Gly	Gly	Asp	Leu	Ser	Asp	Phe	Ile	Thr	Asn	Gly	Glu	Trp	Tyr	Leu	Ile	
198				185				190					195				
199	gga	atg	cca	ggc	aaa	aag	aac	aca	ata	aca	tac	gcg	tgc	tgc	ccc	gag	739
200	Gly	Met	Pro	Gly	Lys	Lys	Asn	Thr	Ile	Thr	Tyr	Ala	Cys	Cys	Pro	Glu	
201	200						205				210				215		
202	ccc	tac	gtg	gac	gtc	acc	ttc	acc	atc	atg	ata	aga	aga	cga	acc	ttg	787
203	Pro	Tyr	Val	Asp	Val	Thr	Phe	Thr	Ile	Met	Ile	Arg	Arg	Arg	Thr	Leu	
204					220					225				230			
205	tac	tac	ttc	ttc	aac	ctg	atc	gtc	ccg	tgc	gtg	ctg	atc	tca	tcg	atg	835
206	Tyr	Tyr	Phe	Phe	Asn	Leu	Ile	Val	Pro	Cys	Val	Leu	Ile	Ser	Ser	Met	
207				235				240					245				
208	gca	ctc	ctc	ggc	ttc	aca	ctg	cca	cca	gac	tcc	gga	gag	aaa	ctc	aca	883
209	Ala	Leu	Leu	Gly	Phe	Thr	Leu	Pro	Pro	Asp	Ser	Gly	Glu	Lys	Leu	Thr	
210				250				255					260				
211	ctt	gga	gtc	act	att	ctt	cta	tcg	ctg	acg	gtg	ttc	ctc	aac	ctg	gta	931
212	Leu	Gly	Val	Thr	Ile	Leu	Leu	Ser	Leu	Thr	Val	Phe	Leu	Asn	Leu	Val	
213				265				270					275				
214	gcc	gag	acc	ctg	cca	cag	gtc	tcc	gac	gct	atc	ccc	ctg	tta	ggg	acg	979
215	Ala	Glu	Thr	Leu	Pro	Gln	Val	Ser	Asp	Ala	Ile	Pro	Leu	Leu	Gly	Thr	
216	280					285				290				295			
217	tac	ttc	aat	tgc	atc	atg	ttc	atg	gta	gcg	tcg	tct	gtg	gta	ctg	act	1027
218	Tyr	Phe	Asn	Cys	Ile	Met	Phe	Met	Val	Ala	Ser	Ser	Val	Val	Leu	Thr	
219				300				305					310				
220	gtg	gtg	gta	ctc	aat	tac	cac	cat	cga	aca	gct	gat	ata	cat	gaa	atg	1075
221	Val	Val	Val	Leu	Asn	Tyr	His	His	Arg	Thr	Ala	Asp	Ile	His	Glu	Met	
222				315				320					325				
223	cca	cag	tgg	ata	aaa	tca	gta	ttc	cta	caa	tgg	ttg	cca	tgg	ata	ctg	1123
224	Pro	Gln	Trp	Ile	Lys	Ser	Val	Phe	Leu	Gln	Trp	Leu	Pro	Trp	Ile	Leu	
225				330				335					340				
226	cga	atg	tcg	agg	cca	ggg	aag	aag	atc	acc	agg	aag	act	ata	atg	atg	1171
227	Arg	Met	Ser	Arg	Pro	Gly	Lys	Lys	Ile	Thr	Arg	Lys	Thr	Ile	Met	Met	
228				345				350					355				
229	aac	acg	agg	atg	agg	gag	ctg	gaa	ctg	aag	gag	agg	tcg	tcg	aag	tcc	1219
230	Asn	Thr	Arg	Met	Arg	Glu	Leu	Glu	Leu	Lys	Glu	Arg	Ser	Ser	Lys	Ser	
231	360					365				370				375			
232	ttg	ctg	gcg	aat	gtt	cta	gat	att	gat	gat	gac	ttc	aga	cac	ggc	cct	1267
233	Leu	Leu	Ala	Asn	Val	Leu	Asp	Ile	Asp	Asp	Asp	Phe	Arg	His	Gly	Pro	
234				380						385				390			
235	ccg	cct	cct	aac	agt	act	gcc	tcg	acc	ggg	aat	ttg	gga	cct	ggg	tgc	1315
236	Pro	Pro	Pro	Asn	Ser	Thr	Ala	Ser	Thr	Gly	Asn	Leu	Gly	Pro	Gly	Cys	
237				395				400					405				
238	tca	ata	ttc	cg	acg	gat	ttc	cgt	cgg	tcg	ttc	gtc	cgt	ccg	tcc	acg	1363

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241	atg gaa gac gtg ggc ggc ggg ctg ggt agc cac cat cgc gag ctg cac	1411
242	Met Glu Asp Val Gly Gly Gly Leu Gly Ser His His Arg Glu Leu His	
243	425 430 435	
244	ctc ata ctg aga gag ctg cag ttc atc acg gcc agg atg aag aag gct	1459
245	Leu Ile Leu Arg Glu Leu Gln Phe Ile Thr Ala Arg Met Lys Lys Ala	
246	440 445 450 455	
247	gat gag gaa gcc gag ctg atc agc gac tgg aag ttt gct gcg atg gtt	1507
248	Asp Glu Glu Ala Glu Leu Ile Ser Asp Trp Lys Phe Ala Ala Met Val	
249	460 465 470	
250	gtt gat agg ttt tgc ctg ttc gtg ttc aca ctt ttc aca atc atc gcg	1555
251	Val Asp Arg Phe Cys Leu Phe Val Phe Thr Leu Phe Thr Ile Ile Ala	
252	475 480 485	
253	aca gta gct gtc ctg tta tgc gca ccg cat atc atc gtg caa	1597
254	Thr Val Ala Val Leu Leu Ser Ala Pro His Ile Ile Val Gln	
255	490 495 500	
256	tgaaccaacc actgagccgg caactccggc gcatgaatga gagaaataat tattagatcg	1657
257	ccgatttgta attataattg ataatgtaat taaattaaat acgtggttga aacgcacacg	1717
258	tctccataac aaagtcttaa gacattaaat tatgataaat ttacatattg tagttaagtc	1777
259	gagtgttgat ggaaatttta gccggcgcaa ggagtctctg gaaggctctg atatatTTTT	1837
260	tcttattgtt gtatattgta tcgttgttca tgttttcttt caggaaagtga gctttgtact	1897
261	gtttgtttct tcgatggcag gtgcacttca gttcaggctg aaatttccat taacattttat	1957
262	ttaaacaat gtgatgttga ctaggatgtt atacagataa atgttgacgt gtataatttg	2017
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under new
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Gln Gln Leu Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His
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*This is a
print of the entire
file - file was
printed for exploratory
purpose.*

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9

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16

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when is sequence 2? per sequence
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 Leu Glu Trp Asn Asp Met Asn Leu Arg Trp Asn Thr Ser Asp Phe Gly
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 Gly Val Lys Asp Leu Arg Val Pro Pro His Arg Leu Trp Lys Pro Asp
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Sequences
only are
in the
file, please
number
them
1, 2, 3.

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(see next page)

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